Freeform Search

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: l1 and cDNA

Display: 10 **Documents in Display Format:** - **Starting with Number** 1

Generate: ○ **Hit List** ◉ **Hit Count** ○ **Side by Side** ○ **Image**

Search | Clear | Interrupt

Search History

DATE: Wednesday, April 21, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L4	L3 and single stand binding protein	0	L4
L3	l1 and cDNA	1	L3
L2	l1 and (taq polymerase or reverse transcriptase)	0	L2
L1	5593834.pn.	2	L1

END OF SEARCH HISTORY

Freeform Search

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: L9 and single strand binding protein

Display: 10 **Documents in Display Format:** - **Starting with Number** 21

Generate: ○ **Hit List** ◉ **Hit Count** ○ **Side by Side** ○ **Image**

Search Clear Interrupt

Search History

DATE: Wednesday, April 21, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L10	L9 and single strand binding protein	1	L10
L9	baugh.in.	755	L9
L8	L7 and single strand binding protein	1	L8
L7	hunter.in.	7024	L7
L6	L5 and cDNA	24	L6
L5	L4 and reverse transcri$7	24	L5
L4	taq polymerase and single strand binding protein	38	L4
L3	taq polymerase and T4GP32	0	L3
L2	taq polymerase same single strand binding protein	0	L2
L1	taq polymerase same single-strand binding protein same reverse transcri$7	0	L1

END OF SEARCH HISTORY

10038177

* * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 14:54:48 ON 21 APR 2004

=> file medline caplus biosis embase

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 14:55:03 ON 21 APR 2004

FILE 'CAPLUS' ENTERED AT 14:55:03 ON 21 APR 2004
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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FILE 'BIOSIS' ENTERED AT 14:55:03 ON 21 APR 2004

FILE 'EMBASE' ENTERED AT 14:55:03 ON 21 APR 2004

=> s tag polymerase# (P) (single strand binding protein# or RecA)
L1 1 TAG POLYMERASE# (P) (SINGLE STRAND BINDING PROTEIN# OR RECA)

=> s l1 and reverse transcriptase#
L2 0 L1 AND REVERSE TRANSCRIPTASE#

=> s l1 and CENA
L3 0 L1 AND CENA

=> s l1 and cDNA
L4 0 L1 AND CDNA

=> d l1 bib ab kwic

L1 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:446729 CAPLUS
DN 122:180284
TI Improvement of nucleic acid reactions involving cycling between single- and double-stranded nucleic acids with single- and double-stranded binding ligands
IN Lane, Michael J.; Benight, Albert S.; Faldasz, Brian D.
PA Research Foundation of State University of New York, USA
SO PCT Int. Appl., 76 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9500666	A1	19950105	WO 1994-US6800	19940616
	W: AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, ES, FI, GB, GE, HU, JP, KE, KG, KP, KR, KZ, LK, LU, LV, MD, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, UZ, VN				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	CA 2165544	AA	19950105	CA 1994-2165544	19940616
	AU 9472083	A1	19950117	AU 1994-72083	19940616
	EP 708839	A1	19960501	EP 1994-921308	19940616
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	US 5593834	A	19970114	US 1995-427863	19950426
	US 6027884	A	20000222	US 1996-763417	19961211
PRAI	US 1993-78759		19930617		

US 1993-153535 19931117
US 1994-224840 19940408
US 1994-260200 19940616
WO 1994-US6800 19940616

AB The title improvement comprises providing for thermodn. rather than thermal cycling and thereby allowing the reaction to proceed under isothermal conditions. The thermodn. cycling is provided for by including in the reaction a balanced mixture of single-strand and duplex nucleic acid binding ligands to insure that the reaction (formation of duplex from single-stranded nucleic acid) proceeds in both directions at rates which allow the production of a significant level of a desired product. Inclusion of an appropriate level of single-strand binding ligand can also result in more selective hybridization and thus allow greater selectivity in hybridization-based reactions. The concept was applied to PCR and allowed isothermal PCR to be demonstrated. **Tag polymerase** and **single-strand binding protein** were used as the double-stranded and single-stranded DNA binding proteins, resp.

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```
=> s transcriptase(P)(single strand binding protein or RecA)
L5          43 TRANSCRIPTASE(P)(SINGLE STRAND BINDING PROTEIN OR RECA)

=> s l5 and (produc### or mak### or synthesiz###)(10a)cDNA
L6           0 L5 AND (PRODUC### OR MAK### OR SYNTHESIZ###)(10A) CDNA

=> s l5 and (amplif###### (10a)cDNA
UNMATCHED LEFT PARENTHESIS 'AND (AMPLIF####'
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> s l5 and (amplif#######(10a)cDNA)
L7           0 L5 AND (AMPLIF#######(10A) CDNA)

=> s l5 and cDNA
L8           3 L5 AND CDNA

=> dup rem l8
PROCESSING COMPLETED FOR L8
L9           3 DUP REM L8 (0 DUPLICATES REMOVED)

=> d l9 1-3 bib ab kwic

L9   ANSWER 1 OF 3  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2003:971610  CAPLUS
DN   140:24132
TI   DNA polymerase mutants with increased reverse transcriptase activity
IN   Arezi, Bahram; Hogrefe, Holly; Sorge, Joseph A.; Hansen, Connie Jo
PA   Stratagene, USA
SO   U.S. Pat. Appl. Publ., 51 pp., Cont.-in-part of U.S. Ser. No. 223,650.
```

CODEN: USXXCO
DT Patent
LA English
FAN.CNT 5

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2003228616	A1	20031211	US 2003-435766	20030512
WO 2001032887	A1	20010510	WO 2000-US29706	20001027
W: AU, CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 2003157483	A1	20030821	US 2001-896923	20010629
US 2004009486	A1	20040115	US 2002-223650	20020819
PRAI US 1999-162600P	P	19991029		
US 2000-698341	A2	20001027		
WO 2000-US29706	A	20001027		
US 2001-896923	A2	20010629		
US 2002-223650	A2	20020819		

AB The invention relates to the discovery of thermostable DNA polymerases, e.g., Archaeal DNA polymerases, that bear one or more mutations resulting in increased reverse transcriptase activity relative to their unmodified wild-type forms. Wildtype (exo+) JDF-3 DNA polymerase and JDF-3 DNA polymerase substantially lacking 3'-5' exonuclease activity (exo) were prepared Point mutations phenylalanine (F), tyrosine (Y), and tryptophan (W) were introduced at leucine (L) 409 of exo- and exo+Pfu and at L408 of exo- and exo+JDF-3 DNA polymerases using the Quikchange site directed mutagenesis kit (Stratagene). Partially purified prepns. of the exo- and exo+ JDF-3 L408F and L408Y and Pfu L409F and L409Y showed improved RT activity compared to wild type JDF-3 and Pfu. Purified prepns. of the exo-JDF-3 L408H and L408F showed improved RT activity compared to wild type JDF-3 and Pfu. The results demonstrate that adding DMSO significantly improves the reverse transcriptase activity of exo+ Pfu L409Y.

IT Protein sequences
cDNA sequences
(DNA polymerase mutants with increased reverse transcriptase activity)

IT Enzymes, biological studies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(**RecA**, fusion products with DNA polymerases; DNA polymerase mutants with increased reverse **transcriptase** activity)

L9 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:666860 CAPLUS
DN 133:262243
TI Improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning
IN Pelletier, Jerry
PA McGill University, Can.
SO PCT Int. Appl., 43 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000055307	A2	20000921	WO 2000-CA261	20000310
W: CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 1165760	A2	20020102	EP 2000-908881	20000310
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 2002119467	A1	20020829	US 2001-954512	20010912

PRAI US 1999-124011P P 19990312
WO 2000-CA261 W 20000310

AB The present invention relates to genetic engineering, and especially to **cDNA** synthesis and **cDNA** cloning. More specifically, a method is presented for increasing the processivity of a DNA- or RNA-dependent RNA- or DNA-polymerase comprising an addition of a general nucleic acid binding protein. In particular, the present invention relates to methods for increasing the processivity of reverse **transcriptase** (RT) E. coli DNA polymerase and T7 DNA polymerase using a nucleic acid binding protein such as Ncp7, **recA**, SSB and T4gp32. The invention further relates to assays to identify and select agents capable of increasing the processivity of a DNA or RNA-dependent polymerase, such as MMTV RT, AMV RT, T7 DNA polymerase and E. coli DNA polymerase. In a particularly preferred embodiment, the invention relates to a method for increasing the generation of full-length **cDNA** clones using a nucleic acid binding protein such as Ncp7, **recA**, SSB and T4gp32.

TI Improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning

AB The present invention relates to genetic engineering, and especially to **cDNA** synthesis and **cDNA** cloning. More specifically, a method is presented for increasing the processivity of a DNA- or RNA-dependent RNA- or DNA-polymerase comprising an addition of a general nucleic acid binding protein. In particular, the present invention relates to methods for increasing the processivity of reverse **transcriptase** (RT) E. coli DNA polymerase and T7 DNA polymerase using a nucleic acid binding protein such as Ncp7, **recA**, SSB and T4gp32. The invention further relates to assays to identify and select agents capable of increasing the processivity of a DNA or RNA-dependent polymerase, such as MMTV RT, AMV RT, T7 DNA polymerase and E. coli DNA polymerase. In a particularly preferred embodiment, the invention relates to a method for increasing the generation of full-length **cDNA** clones using a nucleic acid binding protein such as Ncp7, **recA**, SSB and T4gp32.

ST reverse transcriptase processivity RNA binding protein; DNA polymerase processivity DNA binding protein; **cDNA** cloning polymerase nucleic acid binding protein

IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(DNA-binding; improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning)

IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(NC(p7) (nucleocapsid, p7), of HIV; improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning)

IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(RNA-binding; improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning)

IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(SSB (single-stranded DNA-binding); improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning)

IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)

(gene 32; improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning)

IT Enzymes, biological studies
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(gene recA; improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning)

IT **cDNA**
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning)

IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(nucleocapsid, retroviral; improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning)

IT 9068-38-6, RNA-dependent DNA polymerase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(of MMLV or AMV; improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning)

IT 9012-90-2, DNA-dependent DNA polymerase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(of T7 or E. coli; improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning)

IT 296363-37-6 296363-38-7 296363-39-8
RL: PRP (Properties)
(unclaimed sequence; improving processivity of DNA- or RNA-dependent polymerases with nucleic acid-binding proteins and application to improved **cDNA** cloning)

L9 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:897365 CAPLUS
DN 135:72094
TI RecA-independent ectopic transposition in vivo of a bacterial group II intron
AU Martinez-Abarca, Francisco; Toro, Nicolas
CS Grupo de Ecologia Genetica, Estacion Experimental del Zaidin, Consejo Superior de Investigaciones Cientificas, Granada, 18008, Spain
SO Nucleic Acids Research (2000), 28(21), 4397-4402
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB RmInt1 is a group II intron of Sinorhizobium meliloti which was initially found within the insertion sequence ISRm2011-2. Although the RmInt1 intron-encoded protein lacks a recognizable endonuclease domain, it is able to mediate insertion of RmInt1 at an Intron-specific location in intronless ISRm2011-2 recipient DNA, a phenomenon termed homing. Here we have characterized three addnl. insertion sites of RmInt1 in the genome of S. meliloti. Wo of these sites are within IS elements closely related to ISRm2011-2, which appear to form a characteristic group within the IS630-Tc1 family. The third site is in the oxi1 gene, which encodes a putative oxide reductase. The newly identified integration sites contain

conserved intron-binding site (IBS1 and IB2S) and δ' sequences (14 bp). The RNA of the intron-containing oxi1 gene is able to splice and the oxi1 site is a DNA target for RmInt1 transposition in vivo. Ectopic transposition of RmInt1 into the oxi1 gene occurs at 20-fold lower efficiency than into the homing site (ISRm2011-2) and is independent of the major RecA recombination pathway. The possibility that transposition of RmInt1 to the oxi1 site occurs by reverse splicing into DNA is discussed.

RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

ST Sinorhizobium group II intron transposition; sequence Sinorhizobium intron reverse transcriptase transposase gene oxi1 **cDNA**

IT **cDNA** sequences
(for Sinorhizobium meliloti group II intron reverse transcriptase gene)

IT 9068-38-6, Reverse **transcriptase**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene for; **RecA**-independent ectopic transposition in vivo of a bacterial group II intron)

=>